

From: Chan, Christina
Sent: Wednesday, July 27, 2005 4:01 PM
To: Basi, Nirmal; STIC-Biotech/ChemLib
Subject: RE: Rush search for App. # 10/016,496

Please rush. Thanks Chris

Chris Chan
SPE, 1644
TC 1600 New Hire Training Coordinator
571-272-0841
Remsen 3E89

-----Original Message-----

From: Basi, Nirmal
Sent: Wednesday, July 27, 2005 3:59 PM
To: Chan, Christina
Subject: Rush search for App. # 10/016,496

Christina I am seeking approval for a RUSH sequence search, as indicated below. If approved, could you please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi
Art Unit 1646
Office: Remsen Building, Room 4D68
Mail Room: Remsen Building, room 4C70

Sequence search:

App. #: 10/016,496
Result format: Paper.

Title: POLYCATION-SENSING RECEPTOR IN AQUATIC SPECIES AND METHODS
OF USE THEREOF

Inventors: William Harris et al

Priority Date: 3/27/96
Please search:
i) SEQ ID NOS: 1 and 2

Search issued, commercial databases and pending databases.

Thanks,
Nirmal S. Basi

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 8/1/05
Date Completed: 8/1/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: 1 AA#: 1
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: QDA
WWW/Internet: _____
Other(Specify): _____

RESULT 2
 CDSR HUMAN
 STANDARD, PRT, 1078 AA.
 01-FEB-1995 (Rel. 31, Created)
 01-NOV-1995 (Rel. 32, Last sequence update)
 01-OCT-2004 (Rel. 45, Last annotation update)

DB: Extracellular calcium-sensing receptor precursor (CASR) (Parathyroid
 Cell calcium-sensing receptor).
 GN Name=CASR; Synonyms=GPCR2A, PCAR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pearce S.H.S., Thakker R.V.,
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Parathyroid;
 RX MEDLINE=95279439; PubMed=7759551; DOI=10.1074/jbc.270.21.12919;
 RA Garrett J.B., Capuano I.V., Hammarland L.G., Hung B.C., Brown B.M.,
 RA Hebert S.C., Nemeth B.F., Fuller F.,
 RT "Molecular cloning and functional expression of human parathyroid
 RT calcium receptor cDNAs.",
 RL J. Biol. Chem. 270:12919-12925 (1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=95408281; PubMed=7677761;
 RA Alda K., Kolch S., Tawata M., Onaya T.,
 RT "Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from
 RT human kidney.",
 RL Biochem. Biophys. Res. Commun. 214:524-529 (1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96343809; PubMed=8756555; DOI=10.1210/en.137.9.3842;
 RA Fretchen M., Zink-Lorenz A., Holllosch A., Hafner M., Plockert V.,
 RA Raue F.,
 RT "Expression of a calcium-sensing receptor in a human medullary thyroid
 RT carcinoma cell line and its contribution to calcitonin secretion.",
 RL Endocrinology 137:3842-3848 (1996).
 RN [5]
 RP SEQUENCE OF 643-908 FROM N.A.
 RX MEDLINE=96193893; PubMed=8613532;
 RA Bixle D.D., Ratnam A., Mauro T., Harrie J., Pillai S.,
 RT "Changes in calcium responsiveness and handling during keratinocyte
 RT differentiation. Potential role of the calcium receptor.",
 RL J. Clin. Invest. 97:1085-1093 (1996).
 RN [6]
 RP VARIANTS FHH GLN-185, LYS-297 AND TRP-795.
 RX MEDLINE=94094324; PubMed=7916660;
 RA Pollak M.R., Brown E.M., Chou Y.-H.W., Hebert S.C., Marx S.J.,
 RA Steinmann B., Levy T., Seidman C.B., Seidman J.G.,
 RT "Mutations in the human Ca(2+)-sensing receptor gene cause familial
 RT hypocalcemic hypocalcemia and neonatal severe hyperparathyroidism.",
 RL Cell 75:1297-1303 (1993).
 RN [7]
 RP VARIANTS ADH ALA-127.
 RX MEDLINE=95179179; PubMed=7874174;
 RA Pollak M.R., Brown E.M., Estep H.L., McLaine P.N., Kifor O., Park J.,
 RA Hebert S.C., Seidman C.B., Seidman J.G.,
 RT "Autosomal dominant hypocalcemia caused by a Ca(2+)-sensing receptor
 RT gene mutation.",
 RL Nat. Genet. 8:303-307 (1994).
 RN [8]
 RP VARIANTS FHH MET-62, CYS-66, MET-138, GLU-143 AND GLN-227.
 RX MEDLINE=95243222; PubMed=7726161;
 RA Chou Y.-H.W., Pollak M.R., Brand M.L., T888 G., Argyrakis H.,
 RA Atkinson A.B., Papapoulos S.B., Marx S., Brown E.M., Seidman J.G.,
 RA Seidman C.B.,
 RT "Mutations in the human Ca(2+)-sensing-receptor gene that cause
 RT familial hypocalcemic hypocalcemia.",
 RL Am. J. Hum. Genet. 56:1075-1079 (1995).
 RN [9]
 RP SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.
 RX MEDLINE=95403641; PubMed=7673400; DOI=10.1210/jc.80.9.2594;
 RA Alda K., Kolch S., Inoue M., Nakazato M., Tawata M., Onaya T.,
 RT "Familial hypocalcemic hypocalcemia associated with mutation in the

human Ca(2+)-sensing receptor gene." [10]
 J. Clin. Endocrinol. Metab. 80:2594-2598 (1995).
 RX VARIANT NSHPT LEU-227 AND TTR-582.
 RX MEDLINE=96282293; PubMed=8675635.
 RX Pearce S.H.S., Trump D., Wooding C., Besser G.M., Chew S.L.,
 RA Grant D.B., Heath D.A., Hughes I.A., Paterson C.R., Whyte M.P.,
 RA Thakker R.V.,
 RT "Calcium-sensing receptor mutations in familial benign hypercalcemia
 RT and neonatal hyperparathyroidism." [11]
 J. Clin. Invest. 96:2683-2692 (1995).
 RP VARIANTS FTH THR-116; HIS-681 AND SER-806, AND VARIANT SER-851.
 RX MEDLINE=96311554; PubMed=873126; DOI=10.1093/hmg/5.5.601;
 RA Baron J., Miner K.K., Yanovski J.A., Cunningham A.W., Lane L.,
 RA Zimmerman D., Cutler G.B. Jr.,
 RT "Mutations in the Ca(2+)-sensing receptor gene cause autosomal
 RT dominant and sporadic hypoparathyroidism." [12]
 Hum. Mol. Genet. 5:601-606 (1996).
 RP VARIANT FTH ARG-174.
 RX MEDLINE=97442275; PubMed=929882;
 RX DOI=10.1002/(SICI)1098-1004(1997)10:3<233::AID-HUM9>3.3.CO;2-G;
 RA Ward B.K., Stuckey B.G.A., Gutteridge D.H., Laing N.G., Pullan P.T.,
 RA Ratajczak T.,
 RT "A novel mutation (L174R) in the Ca2+-sensing receptor gene associated
 RT with familial hypocalcemic hypercalcemia." [13]
 Hum. Mutat. 10:233-235 (1997).
 RP VARIANT FTH VAL-616.
 RX MEDLINE=99415602; PubMed=10487661; DOI=10.1210/jc.84.9.3036;
 RA Stock J.L., Brown R.S., Baron J., Codre J.A., Mancilla B.,
 RA De Luca F., Ray K., Mericq M.V.,
 RT "Autosomal dominant hypoparathyroidism associated with short stature
 RT and premature osteoarthritis." [14]
 J. Clin. Endocrinol. Metab. 84:3036-3040 (1999).
 RP VARIANT FTH GLU-557.
 RX MEDLINE=21603857; PubMed=11762699; DOI=10.1385/ENDO.15.3.277;
 RA Nakayama T., Minato W., Nakagawa M., Soma M., Tobe H., Aoi N.,
 RA Koenig K., Sato M., Ozawa Y., Kamatsuse K., Kokubun S.,
 RT "A novel mutation in Ca2+-sensing receptor gene in familial
 RT hypocalcemic hypercalcemia." [15]
 Endocrine 15:277-282 (2001).
 CC -1- FUNCTION: Senses changes in the extracellular concentration of
 CC calcium ions. The activity of this receptor is mediated by a G-
 CC protein that activates a phosphatidylinositol-calcium second
 CC messenger system.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P41180-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P41180-2; Sequence=VSP_002035;
 CC -1- TISSUE SPECIFICITY: Found in kidney, but not in brain, lung,
 CC liver, heart, skeletal muscle, or placenta.
 CC -1- DISEASE: Defects in CASR are the cause of familial hypocalcemic
 CC hypercalcemia, type 1 (FHH) [MIM:145980]; in which the receptor
 CC has reduced activity. FHH is characterized by altered calcium
 CC homeostasis. Affected individuals exhibit mild or modest
 CC hypercalcemia, relative hypocalcemia, and inappropriately normal
 CC PTH levels.
 CC -1- DISEASE: Defects in CASR are the cause of neonatal severe primary
 CC hyperparathyroidism (NSHPT) [MIM:239200]; in which the receptor
 CC has reduced activity. NSHPT is a rare autosomal recessive life-
 CC threatening disorder characterized by very high serum calcium
 CC concentrations, skeletal demineralization, and parathyroid
 CC hyperplasia. In some instances NSHPT has been demonstrated to be
 CC the homozygous form of FHH.
 CC -1- DISEASE: Defects in CASR are the cause of autosomal dominant
 CC hypocalcemia (ADH) [MIM:601198]; in which the receptor is
 CC activated at subnormal Ca(2+) levels.

-1- DISEASE: Defects in CASR are the cause of autosomal dominant
 hypoparathyroidism (FHH) [MIM:146200]. FHH is characterized by
 hypocalcemia and hyperphosphatemia due to inadequate secretion of
 parathyroid hormone. Symptoms are seizures, tetany and cramps.
 -1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
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 CC
 CC EMBL, X81086; CAA56990.1; -
 CC EMBL, U20759; AAA6503.1; -
 CC EMBL, U20760; AAA6504.1; -
 CC EMBL, D50855; BAA09453.1; -
 CC EMBL, S83176; AAB46873.1; -
 CC EMBL, S79217; AAB35262.2; -
 CC EMBL, S68032; AAB29413.2; ALT SEQ.
 CC EMBL, S68033; AAB29414.1; -
 CC EMBL, S68036; AAB29415.1; -
 CC EMBL, S81755; AAD14370.1; -
 CC HSSP, P23385; IEMK.
 CC Gene, HGNC:1514; CASR.
 CC MIM, 601199; -
 CC MIM, 145980; -
 CC MIM, 239200; -
 CC MIM, 601198; -
 CC MIM, 146200; -
 CC GO, GO:0005887; C: integral to plasma membrane; TAS.
 CC GO, GO:0004930; F: G-protein coupled receptor activity; TAS.
 CC GO, GO:0004435; F: phosphoinositide phospholipase C activity; TAS.
 CC GO, GO:0006874; P: calcium ion homeostasis; TAS.
 CC GO, GO:0005513; P: calcium ion sensing; TAS.
 CC GO, GO:0007635; P: chemosensory behavior; TAS.
 CC GO, GO:0007186; P: G-protein coupled receptor protein signal; TAS.
 CC GO, GO:0009653; P: morphogenesis; TAS.
 CC GO, GO:0001503; P: ossification; TAS.
 CC InterPro, IPR001828; ANF receptor.
 CC InterPro, IPR000068; G_Protein_Receptor.
 CC InterPro, IPR000337; GPCR_Mgr.
 CC Pfam, PF00003; Tm_3; 1.
 CC Pfam, PF01094; ANF receptor; 1.
 CC PRINTS, PR00248; GPCRMR.
 CC PROSITE, PS00979; G_PROTEIN_RECP_F3_1; 1.
 CC PROSITE, PS00980; G_PROTEIN_RECP_F3_2; 1.
 CC PROSITE, PS00981; G_PROTEIN_RECP_F3_3; 1.
 CC
 CC Query Match 74.8%; Score 4044.5; DB 1; Length 1078;
 CC Best Local Similarity 74.0%; Pred. No. 2.8e-274;
 CC Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;
 CC
 CC 1 MAOLHQLFLFTLLSIVSVGYGNORAKKDDIILGLPIHFVGAANDDKSRPE 60
 CC 1 MAFLSCCVLLALT-----WHTSAYGPORAKKDDIILGLPIHFVGAANDDKSRPE 56
 CC
 CC 61 ATKICIRNFGFRLOMIFAIRESINNSMTPLPITLGYVIFPDCTVSALETTLSFVA 120
 CC 57 SVSCIRYNFGFRLOMIFAIRESINSSPALPLPLTGYVIFPDCTVSALETTLSFVA 116
 CC
 CC 121 QNKIDSLNLEFCNCSHPISITIAVVGATSGSISTAVANLGLFYIPQVSAASSRLLSN 180
 CC 117 QNKIDSLNLEFCNCSHPISITIAVVGATSGSISTAVANLGLFYIPQVSAASSRLLSN 176
 CC
 CC 181 KMRKATLRTIPDQOQATMAIIEHFQNNVGTAAADDYRPGIDKFRBAVAKDIC 240
 CC 177 KNQFKSPLRTIPDQOQATMAIIEHFQNNVGTAAADDYRPGIDKFRBAVAKDIC 236
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 CC 241 IDSEMSGYVTKOLEFIADVONSAKYIVFSGPDLERLQIVRNITDRITWLAS 300
 CC 237 IDPSELISQVDSBRIQHVVEIVONSTAKYIVFSGPDLERLQIVRNITDRITWLAS 296

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QY 301 EAMASSSLIAEYFHYVGTGTFPALBAGRIEFGNFKLEVPSSRSDNGFVKEFWETP 360
DB 297 EAMASSSLIAMQYFHYVGTGTFPALBAGRIEFGNFKLEVPSSRSDNGFVKEFWETP 356
QY 361 NCYFPEKTLTOLKNSKVPSHGPAQDGSKAGNSRRALRHCCTGEBNITSVETPYLYDT 420
DB 357 NCHLOBGAKGPI---PVDTPLRGHESGDRFNS--STARPLCTGDENISSVETPYLYDT 412
QY 421 HLRISVYVAVYSIAHALODIHSCKEPTGIRANGSCADIKKVEAMOVNHLHLKFTNS 480
DB 413 HLRISVYVAVYSIAHALODIHSCKEPTGIRANGSCADIKKVEAMOVNHLHLKFTNS 472
QY 481 MGEQVDPDQGLKNGVYITINMOLSAEDRSVLEHETGNTAYAKAPSDRINNEKILMG 540
DB 473 MGEQVDPDQGLKNGVYITINMOLSAEDRSVLEHETGNTAYAKAPSDRINNEKILMG 532
QY 541 PSKVVPFNSCSDCVGTRKGIIEGEPGCCFECMACABGSPDENDASACTVCPNDPMN 600
DB 533 PSKVVPFNSCSDCVGTRKGIIEGEPGCCFECMACABGSPDENDASACTVCPNDPMN 592
QY 601 ENHTSCIARIEVLSWTEPFGIALTPAVGLIITSFVLGVFKENTPIVAKTNELAY 660
DB 593 ENHTSCIARIEVLSWTEPFGIALTPAVGLIITSFVLGVFKENTPIVAKTNELAY 652
QY 661 LLIPLSLICR8SSSLIPGEPDWTCLROPAFISFVLICSLIVKTNRLVFEAKIPT 720
DB 653 LLIPLSLICR8SSSLIPGEPDWTCLROPAFISFVLICSLIVKTNRLVFEAKIPT 712
QY 721 SLRHKWGLMQLVPLICILVIVTCLIMLYTAPSPSYNHLDESVIFITCDEGLMA 780
DB 713 SLRHKWGLMQLVPLICILVIVTCLIMLYTAPSPSYNHLDESVIFITCDEGLMA 772
QY 781 LGFLIGYTCLLAALCPFPAPKSRLLPENENAKITTSMLIPFVWISPLPAYVSTYKX 840
DB 773 LGFLIGYTCLLAALCPFPAPKSRLLPENENAKITTSMLIPFVWISPLPAYVSTYKX 832
QY 841 VSAVEVTAIIAASSGGLGCTIYFNKCYIILFKPCNTIIEVYACSTAAHAFVAAATLRS 900
DB 833 VSAVEVTAIIAASSGGLGCTIYFNKCYIILFKPCNTIIEVYACSTAAHAFVAAATLRS 892
QY 901 AASRKRSSSLCGSTISSPASSTCGPG-----LTMEM 931
DB 893 NVSKR8SSSLCGSTISSPASSTCGPG-----LTMEM 952
QY 932 Q-----RCSTQKVSFGSGTFLSLSEFETGRVATLSTKRSKNSADRGDDLP8NH 984
DB 953 QOR8QOQPRCK-QKVFISGTVTFSLSFDEPOKNAMHRNSTHONSLEAKSSDTLTH- 1010
QY 985 DQ8PPQKCEPOPANDARYKAAFTKLTLESPPGSKERP 1021
DB 1011 -----QPLPLQCCGTDLDLTVOETGLQGPVGGDQRP 1042

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RESULT 3
ID CASR_BOVIN STANDARD; PRT; 1085 AA.
AC P35384;
DT 01-JUN-1994 (Rel. 29, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Extracellular calcium-sensing receptor precursor (CASR) (Parathyroid
GN Name=CASR; Synonyms=GPRC2A, PCAR1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN (1)
RC SEQUENCE FROM N.A.
RC TISSUE=Parathyroid;
RX MEDLINE=94077182; PubMed=8255296; DOI=10.1038/366575a0;

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RA Brown & M., Gamba G., Riccardi D., Lombardi M., Butters R., Klor O.,
 RA Sun A., Hediger M.A., Lytton J., Hebert S.C.,
 RT "Cloning and characterization of an extracellular Ca(2+)-sensing
 RL receptor from bovine parathyroid.";
 RL Nature 366:575-580(1993).
 CC -1- FUNCTION: Senses changes in the extracellular concentration of
 CC calcium ions. The activity of this receptor is mediated by a G-
 CC protein that activates a phosphatidylinositol-calcium second
 CC messenger system.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
 CC
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 CC modified and this statement is not removed. Usage by and for commercial
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CC EMBL: S67307; AA29171.1; -.
 CC PIR: S40476; S40476.
 CC HSSP: P23385; 1EWT.
 CC InterPro: IPR001828; ANF receptor.
 CC InterPro: IPR000068; Ca_sens receptor.
 CC InterPro: IPR000337; GPCR_MgR.
 CC Pfam: PF00003; 7tm_3; 1.
 CC Pfam: PF01094; ANF_receptor; 1.
 CC PRINTS: PR00248; GPCR_MgR.
 CC PROSITE: PS00979; G_PROTEIN_RECP_F3_1; 1.
 CC PROSITE: PS00980; G_PROTEIN_RECP_F3_2; 1.
 CC PROSITE: PS00981; G_PROTEIN_RECP_F3_3; 1.
 CC PROSITE: PS0259; G_PROTEIN_RECP_F3_4; 1.
 CC G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
 CC
 CC CHAIN 1 19
 CC FT SIGNAL 20 1085
 CC FT CHAIN 20 613
 CC FT DOMAIN 614 636
 CC FT TRANSMEM 637 650
 CC FT DOMAIN 651 671
 CC FT TRANSMEM 672 682
 CC FT DOMAIN 683 701
 CC FT TRANSMEM 702 725
 CC FT TRANSMEM 726 746
 CC FT DOMAIN 747 770
 CC FT TRANSMEM 771 793
 CC FT DOMAIN 807 829
 CC FT TRANSMEM 830 837
 CC FT DOMAIN 838 863
 CC FT TRANSMEM 864 1085
 CC FT DOMAIN 91 91
 CC FT CARBOHYD 131 131
 CC FT CARBOHYD 262 262
 CC FT CARBOHYD 288 288
 CC FT CARBOHYD 401 401
 CC FT CARBOHYD 447 447
 CC FT CARBOHYD 469 469
 CC FT CARBOHYD 489 489
 CC FT CARBOHYD 542 542
 CC FT CARBOHYD 595 595
 CC SEQUENCE 1085 AA; 121170 MW; 5D6DB8C9CD1B47 CRC64;

Query Match 73.94; Score 3999.5; DB 1; Length 1085;
 Best Local Similarity 72.81; Pred. No. 4e-271;
 Matches 778; Conservative 92; Mismatches 141; Indels 57; Gaps 8;
 QY 1 MAQLHQLLFTGFTLLSYVNGYGNQRAQKQKDIILGSLPIHFGVAARDQDKSRPE 60
 DB 1 MALVSCCHLLAFS---TWTSAYGPDRAKQKDDIILGSLPIHFGVAARDQDKSRPE 57
 QY 61 ATKCIKRVNFGFRWLOAMIFAIIEINSMFTLPNTTAYRIPTDCNTYSKALENTLSFVA 120

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Db 58 SVEICIRYNGFRMLOAMI PAIEINSSPALLPMTLGRIDTCNTVSKALEATLSFVA 117
Qy 121 ONKIDSLDDEFNCSDHI PSTIAVVGATGSGISTAVANLGLFYIPOVYASSSRLSN 180
Db 118 ONKIDSLDDEFNCSEHI PSTIAVVGATGSGISTAVANLGLFYIPOVYASSSRLSN 177
Qy 181 KNEYKAFLETPNDEQOATAMABITENHOMVGTGLAADDDYGRPGIDKPREBAVKDIC 240
Db 178 KNEYKAFLETPNDEQOATAMABITENHOMVGTGLAADDDYGRPGIDKPREBAVKDIC 237
Qy 241 IDSEMILOYTOKLEFIADVIONSAKVIVVSNBDEPLLOEYRENTDRIWLAS 300
Db 238 IDSEMILOYTOKLEFIADVIONSAKVIVVSNBDEPLLOEYRENTDRIWLAS 297
Qy 301 EAAASSLLAKPEYFHVVGTTGFPALPAGRI PGFNKELKEVHPSRSDNGFVFEWETP 360
Db 298 EAAASSLLAKPEYFHVVGTTGFPALPAGRI PGFNKELKEVHPSRSDNGFVFEWETP 357
Qy 361 NCYFEKTLTQLKNSVPSHGPAAQDGSANNSRTALRHPTGBENITVETPYLDYT 420
Db 358 NCYFEKTLTQLKNSVPSHGPAAQDGSANNSRTALRHPTGBENITVETPYLDYT 413
Qy 421 HIRISYVAVYVSIHALODIHSCKRGNGIPANGSCADIKKREANQVNLHLKFTNS 480
Db 414 HIRISYVAVYVSIHALODIHSCKRGNGIPANGSCADIKKREANQVNLHLKFTNS 473
Qy 481 MGEYDPPDQDLKKNYTIINQLSADESVLFHEVGNAYAKOSDRINEXKILWSG 540
Db 474 MGEYDPPDQDLKKNYTIINQLSADESVLFHEVGNAYAKOSDRINEXKILWSG 533
Qy 541 FSKVVPFNSCRDVCPTRGKIIIEGPTCCFPCMA CAGEFSDENDASACTCPDNFSN 600
Db 534 FSKVVPFNSCRDVCPTRGKIIIEGPTCCFPCMA CAGEFSDENDASACTCPDNFSN 593
Qy 601 ENHNSCIAKEIETSWTEPFGLTIFPAVLGILLTSPTLGPFIKRNTPYKATNRELISY 660
Db 594 ENHNSCIAKEIETSWTEPFGLTIFPAVLGILLTSPTLGPFIKRNTPYKATNRELISY 653
Qy 661 LILFSLICCFSSSIFIGBPDMTCRLQAPAGISFVLCISCIIVKTNRLVFEAKIPT 720
Db 654 LILFSLICCFSSSIFIGBPDMTCRLQAPAGISFVLCISCIIVKTNRLVFEAKIPT 713
Qy 721 SLRKNVGNLLOPLVLCILVQVTCIIMLYTAPSSSYNHELEDEVIETCDGSLMA 780
Db 714 SLRKNVGNLLOPLVLCILVQVTCIIMLYTAPSSSYNHELEDEVIETCDGSLMA 773
Qy 781 LGLIGVTCILAAICFPFAKSRKLPENFEAKPTSMILPFIWISFIPAVYSTYGR 840
Db 774 LGLIGVTCILAAICFPFAKSRKLPENFEAKPTSMILPFIWISFIPAVYSTYGR 833
Qy 841 VSAVEYIAIASSFGILGCTYFNKCYIIIFKPCRNTEIEVRGTAHAAPVARATLRS 900
Db 834 VSAVEYIAIASSFGILGCTYFNKCYIIIFKPCRNTEIEVRGTAHAAPVARATLRS 893
Qy 901 AASRKSLSLGGSTISSPASSTG-----P 925
Db 894 AASRKSLSLGGSTISSPASSTG-----P 925
Qy 926 GLTMEQO-----RSTOKVSGSGTYTLISFETGXYATLSTARSNSADGRSGD 978
Db 954 PESTPOPOQOPQPPRK-OKVIFGSGTVFSLSFEBPOTAAVHNSTHQTSLMAQNND 1012
Qy 979 LPSRHDOGPPOKCEBOPANDARYKAPKGTLESFGSKENPTMEE 1026
Db 1013 LPSRHDOGPPOKCEBOPANDARYKAPKGTLESFGSKENPTMEE 1053

```

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RESULT 4
CASR_RAT STANDARD; PRT; 1079 AA.
AC P48442;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

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DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Extracellular calcium-sensing receptor precursor (CASR) (Parathyroid
DE Cell calcium-sensing receptor)
GN Name=Casr; Synonyms=Gprc2a, Pcalr;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney outer medulla;
RX MEDLINE=95241465; PubMed=7724534;
RA Riccardi D., Park J., Lee W., Gambo G., Brown E.M., Hebert S.C.,
RT "Cloning and functional expression of a rat kidney extracellular
RT calcium/polyvalent cation-sensing receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
RN [2]
RP SEQUENCE OF 1-294 FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=95241465; PubMed=7724534;
RA Ruat M., Snowman A.M., Snyder S.H.,
RT "Calcium sensing receptor: molecular cloning in rat and localization
RT to nerve terminals."
RL Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).
CC -1- FUNCTION: Senses changes in the extracellular concentration of
CC calcium ions. The activity of this receptor is mediated by a G-
CC protein that activates a phosphatidylinositol-calcium second
CC messenger system.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
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CC
DR EMBL: U01354; AAC52149.1;
DR EMBL: U20289; AAC52195.1;
DR PIR: I59362; I59362.
DR HSSP: P23385; IEMX.
DR RGD: 2277; Casr.
DR InterPro: IPR001828; ANP_receptor.
DR InterPro: IPR000068; Ca_sens_receptor.
DR InterPro: IPR000337; GPCR_Mgr.
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DR PROSITE: PS01259; G_PROTEIN_RECP_F3_281; 1.
DR PROSITE: PS01260; G_PROTEIN_RECP_F3_282; 1.
DR PROSITE: PS01261; G_PROTEIN_RECP_F3_283; 1.
DR PROSITE: PS01262; G_PROTEIN_RECP_F3_284; 1.
DR PROSITE: PS01263; G_PROTEIN_RECP_F3_285; 1.
DR PROSITE: PS01264; G_PROTEIN_RECP_F3_286; 1.
DR PROSITE: PS01265; G_PROTEIN_RECP_F3_287; 1.
DR PROSITE: PS01266; G_PROTEIN_RECP_F3_288; 1.
DR PROSITE: PS01267; G_PROTEIN_RECP_F3_289; 1.
DR PROSITE: PS01268; G_PROTEIN_RECP_F3_290; 1.
DR PROSITE: PS01269; G_PROTEIN_RECP_F3_291; 1.
DR PROSITE: PS01270; G_PROTEIN_RECP_F3_292; 1.
DR PROSITE: PS01271; G_PROTEIN_RECP_F3_293; 1.
DR PROSITE: PS01272; G_PROTEIN_RECP_F3_294; 1.
DR PROSITE: PS01273; G_PROTEIN_RECP_F3_295; 1.
DR PROSITE: PS01274; G_PROTEIN_RECP_F3_296; 1.
DR PROSITE: PS01275; G_PROTEIN_RECP_F3_297; 1.
DR PROSITE: PS01276; G_PROTEIN_RECP_F3_298; 1.
DR PROSITE: PS01277; G_PROTEIN_RECP_F3_299; 1.
DR PROSITE: PS01278; G_PROTEIN_RECP_F3_300; 1.
DR PROSITE: PS01279; G_PROTEIN_RECP_F3_301; 1.
DR PROSITE: PS01280; G_PROTEIN_RECP_F3_302; 1.
DR PROSITE: PS01281; G_PROTEIN_RECP_F3_303; 1.
DR PROSITE: PS01282; G_PROTEIN_RECP_F3_304; 1.
DR PROSITE: PS01283; G_PROTEIN_RECP_F3_305; 1.
DR PROSITE: PS01284; G_PROTEIN_RECP_F3_306; 1.
DR PROSITE: PS01285; G_PROTEIN_RECP_F3_307; 1.
DR PROSITE: PS01286; G_PROTEIN_RECP_F3_308; 1.
DR PROSITE: PS01287; G_PROTEIN_RECP_F3_309; 1.
DR PROSITE: PS01288; G_PROTEIN_RECP_F3_310; 1.
DR PROSITE: PS01289; G_PROTEIN_RECP_F3_311; 1.
DR PROSITE: PS01290; G_PROTEIN_RECP_F3_312; 1.
DR PROSITE: PS01291; G_PROTEIN_RECP_F3_313; 1.
DR PROSITE: PS01292; G_PROTEIN_RECP_F3_314; 1.
DR PROSITE: PS01293; G_PROTEIN_RECP_F3_315; 1.
DR PROSITE: PS01294; G_PROTEIN_RECP_F3_316; 1.
DR PROSITE: PS01295; G_PROTEIN_RECP_F3_317; 1.
DR PROSITE: PS01296; G_PROTEIN_RECP_F3_318; 1.
DR PROSITE: PS01297; G_PROTEIN_RECP_F3_319; 1.
DR PROSITE: PS01298; G_PROTEIN_RECP_F3_320; 1.
DR PROSITE: PS01299; G_PROTEIN_RECP_F3_321; 1.
DR PROSITE: PS01300; G_PROTEIN_RECP_F3_322; 1.
DR PROSITE: PS01301; G_PROTEIN_RECP_F3_323; 1.
DR PROSITE: PS01302; G_PROTEIN_RECP_F3_324; 1.
DR PROSITE: PS01303; G_PROTEIN_RECP_F3_325; 1.
DR PROSITE: PS01304; G_PROTEIN_RECP_F3_326; 1.
DR PROSITE: PS01305; G_PROTEIN_RECP_F3_327; 1.
DR PROSITE: PS01306; G_PROTEIN_RECP_F3_328; 1.
DR PROSITE: PS01307; G_PROTEIN_RECP_F3_329; 1.
DR PROSITE: PS01308; G_PROTEIN_RECP_F3_330; 1.
DR PROSITE: PS01309; G_PROTEIN_RECP_F3_331; 1.
DR PROSITE: PS01310; G_PROTEIN_RECP_F3_332; 1.
DR PROSITE: PS01311; G_PROTEIN_RECP_F3_333; 1.
DR PROSITE: PS01312; G_PROTEIN_RECP_F3_334; 1.
DR PROSITE: PS01313; G_PROTEIN_RECP_F3_335; 1.
DR PROSITE: PS01314; G_PROTEIN_RECP_F3_336; 1.
DR PROSITE: PS01315; G_PROTEIN_RECP_F3_337; 1.
DR PROSITE: PS01316; G_PROTEIN_RECP_F3_338; 1.
DR PROSITE: PS01317; G_PROTEIN_RECP_F3_339; 1.
DR PROSITE: PS01318; G_PROTEIN_RECP_F3_340; 1.
DR PROSITE: PS01319; G_PROTEIN_RECP_F3_341; 1.
DR PROSITE: PS01320; G_PROTEIN_RECP_F3_342; 1.
DR PROSITE: PS01321; G_PROTEIN_RECP_F3_343; 1.
DR PROSITE: PS01322; G_PROTEIN_RECP_F3_344; 1.
DR PROSITE: PS01323; G_PROTEIN_RECP_F3_345; 1.
DR PROSITE: PS01324; G_PROTEIN_RECP_F3_346; 1.
DR PROSITE: PS01325; G_PROTEIN_RECP_F3_347; 1.
DR PROSITE: PS01326; G_PROTEIN_RECP_F3_348; 1.
DR PROSITE: PS01327; G_PROTEIN_RECP_F3_349; 1.
DR PROSITE: PS01328; G_PROTEIN_RECP_F3_350; 1.
DR PROSITE: PS01329; G_PROTEIN_RECP_F3_351; 1.
DR PROSITE: PS01330; G_PROTEIN_RECP_F3_352; 1.
DR PROSITE: PS01331; G_PROTEIN_RECP_F3_353; 1.
DR PROSITE: PS01332; G_PROTEIN_RECP_F3_354; 1.
DR PROSITE: PS01333; G_PROTEIN_RECP_F3_355; 1.
DR PROSITE: PS01334; G_PROTEIN_RECP_F3_356; 1.
DR PROSITE: PS01335; G_PROTEIN_RECP_F3_357; 1.
DR PROSITE: PS01336; G_PROTEIN_RECP_F3_358; 1.
DR PROSITE: PS0133
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FT CARBOHYD 130 130 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 261 261 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 287 287 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 366 366 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 446 446 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 468 468 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 488 488 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 541 541 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 594 594 N-linked (GlcNAc...) (potential)
 SQ SEQUENCE 1079 AA, 120867 MW, D766450361F9736 CRC64;

Query Match 73.9%; Score 3996; DB 1; Length 1079;
 Best Local Similarity 73.7%; Pred. No. 6,9e-271;
 Matches 780; Conservative 85; Mismatches 140; Indels 54; Gaps 8;

QY 1 MAQLHCOLLFLGFTLLQSYNGVGNQRAQKGDIIILGLFPIHFVGAADQDLKSRE 60
 DB 1 MASYSCCLALAL-----AMHSAAGPDPQAKKKGDIILGLFPIHFVGAADQDLKSRE 56
 QY 61 ATKIRNPNPGRFRLQAMIFALIEINNSMTPLNITIGRIEDTCNTVSKALEATLSFVA 120
 DB 57 SVECIIRNPNPGRFRLQAMIFALIEINNSMTPLNITIGRIEDTCNTVSKALEATLSFVA 116
 QY 121 QNKISLNDERFNCSDHIPSTIAVVGATGSGISTAVANLGLFYIPQVYASSRLLSN 180
 DB 117 QNKISLNDERFNCSDHIPSTIAVVGATGSGISTAVANLGLFYIPQVYASSRLLSN 176
 QY 181 KNEYKAFLEKTIIPNDEQATAMAEIIIEHFQNNVGTLAADDYGRPGIDKREBEAVKRDIC 240
 DB 177 KNEYKAFLEKTIIPNDEQATAMAEIIIEHFQNNVGTLAADDYGRPGIDKREBEAERDIC 236
 QY 241 IDFSMISQYTKQKLEFIADYTONSSAAYVYVPSNGPLLELLOEYRNRITDTIMAS 300
 DB 237 IDFSMISQYTKQKLEFIADYTONSSAAYVYVPSNGPLLELLOEYRNRITDTIMAS 296
 QY 301 EAMASSSLIAKPEYFHVVGITGIPALRAGRIPGNKFLKREVPSSSDNGFVKEEMSETP 360
 DB 237 EAMASSSLIAKPEYFHVVGITGIPALRAGRIPGNKFLKREVPSSSDNGFVKEEMSETP 356
 QY 361 NCYFTEKTLTQK-NSKVPSHGPAAGDGSKAGNSRRALRHPGTGEENITSVETPYLDY 419
 DB 357 NCHLQEGAKGPLPVDTFVRSH-----EEGGRLLNS-STAFRPLCTGDEINISVETPYMDY 411
 QY 420 THLRISYNYVAVYGIHALODIHSCKRGTGIPANGSCADIKKGAQVYANLHLKXTN 479
 DB 412 THLRISYNYVAVYGIHALODIHSCKRGTGIPANGSCADIKKGAQVYANLHLKXTN 471
 QY 480 SMGQVDPDQDGLKGNATYIIMQSAEDSVLPFHVGNVYNAKPSDRILNINEKILMS 539
 DB 472 SMGQVDPDQDGLKGNATYIIMQSAEDSVLPFHVGNVYNAKPSDRILNINEKILMS 531
 QY 540 GSKVVPFNSGRCDCVPGTRKGIIEGPTCCFECNACAGEPSDENASACTCPDNFWS 599
 DB 532 GSKVVPFNSGRCDCVPGTRKGIIEGPTCCFECNACAGEPSDENASACTCPDNFWS 591
 QY 600 NENHTSCIAKEIYLSWTERPGIATITPAVLGILITSPYLGFIETPRNTPYKANNRSL 659
 DB 592 NENHTSCIAKEIYLSWTERPGIATITPAVLGILITSPYLGFIETPRNTPYKANNRSL 651
 QY 660 YLLFSLICCFSSSIIFIGEPDMTCRLRQAPAGISFVLCISIVKTNRLVLVEAKIP 719
 DB 652 YLLFSLICCFSSSIIFIGEPDMTCRLRQAPAGISFVLCISIVKTNRLVLVEAKIP 711
 QY 720 TSLHRKVGNLQFLVFLCIVQITCIIMLYTAPSSYRNHLEDEVIFITCDGSLM 779
 DB 712 TSLHRKVGNLQFLVFLCIVQITCIIMLYTAPSSYRNHLEDEVIFITCDGSLM 771
 QY 780 ALGFLIGTCLLAACFPFAFKSRLLPENFNKAKITTSBMLIFVWISFIPAYSTYTGK 839
 DB 772 ALGFLIGTCLLAACFPFAFKSRLLPENFNKAKITTSBMLIFVWISFIPAYSTYTGK 831
 QY 840 FVSAVEVAILAASFGLLGCIYFNKCYIILFPCNNTIEEVASCPAAAFKVAADATLRR 899

DB 832 FVSAVEVAILAASFGLLGCIYFNKCYIILFPCNNTIEEVASCPAAAFKVAADATLRR 891
 QY 900 SAARRRSSSICGTTSPASSSTCGP-----LTME 930
 DB 892 PNIRKSSSSIGSTGSISSSSKNSBDRFPQRPQKQOPLSTOEGQOQOPLTH 951
 QY 931 MQ-----RCSYQKSPFGSGVTLTSLFEEETGRVATLSTRASRNADGRSDULPSR 982
 DB 952 PQOQOQOQOQRC-QXITPSSGVTFTSLSTDEPQKNAMAHNSWRQNSLEAGNSNDTLGR 1010
 QY 983 HHQGPQKCEPOPANDARYAAPTKTLESFGSSKEP 1021
 DB 1011 H-----CALLPLQCADASEMTIQETGLQGPWGDHP 1043

RESULT 5

ID 0802A8 PRELIMINARY; PRF; 1079 AA.
 AC 0802A8;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 OS Calcium sensing receptor.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Dorsal root ganglion;
 RA Bukoski R., Bian K., Wang Y.;
 RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY244122; A059490.1; -
 DR HSSP; P23385; IEMK.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like receptor. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000068; Ca_sens_receptor.
 DR InterPro; IPR000337; GPCR_Mgt.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00592; CASSENSING.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS00979; G_PROTEIN_RECPT_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECPT_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECPT_F3_3; 1.
 DR PROSITE; PS50259; G_PROTEIN_RECPT_F3_4; 1.
 KM Receptor.
 SQ SEQUENCE 1079 AA; 120830 MW; 50A2D026AE65CE81 CRC64;

Query Match 73.7%; Score 3986; DB 2; Length 1079;
 Best Local Similarity 73.5%; Pred. No. 3.5e-270;
 Matches 778; Conservative 87; Mismatches 140; Indels 54; Gaps 8;

QY 1 MAQLHCOLLFLGFTLLQSYNGVGNQRAQKGDIIILGLFPIHFVGAADQDLKSRE 60
 DB 1 MASYSCCLALAL-----AMHSAAGPDPQAKKKGDIILGLFPIHFVGAADQDLKSRE 56
 QY 61 ATKIRNPNPGRFRLQAMIFALIEINNSMTPLNITIGRIEDTCNTVSKALEATLSFVA 120
 DB 57 SVECIIRNPNPGRFRLQAMIFALIEINNSMTPLNITIGRIEDTCNTVSKALEATLSFVA 116
 QY 121 QNKISLNDERFNCSDHIPSTIAVVGATGSGISTAVANLGLFYIPQVYASSRLLSN 180
 DB 117 QNKISLNDERFNCSDHIPSTIAVVGATGSGISTAVANLGLFYIPQVYASSRLLSN 176
 QY 181 KNEYKAFLEKTIIPNDEQATAMAEIIIEHFQNNVGTLAADDYGRPGIDKREBEAVKRDIC 240
 DB 177 KNEYKAFLEKTIIPNDEQATAMAEIIIEHFQNNVGTLAADDYGRPGIDKREBEAERDIC 236